

SEQUENCE LISTING

<110> Susanne LEONHARTSBERGER

Thomas MAIER

<120> METHOD FOR FERMENTATIVE PREPARATION OF S-ADENOSYLMETHIONINE

<130> LEONHARTSBERGER ET AL. - 1

<140> German No. 103 09 856.9

<141> 03-06-2003

<160> 11

<170> PatentIn Ver. 2.0

<210> 1

<211> 384

<212> PRT

<213> Escherichia coli

<400> 1

Met Ala Lys His Leu Phe Thr Ser Glu Ser Val Ser Glu Gly His Pro

1 5 10 15

Asp Lys Ile Ala Asp Gln Ile Ser Asp Ala Val Leu Asp Ala Ile Leu

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Glu Gln Asp Pro Lys Ala Arg Val Ala Cys Glu Thr Tyr Val Lys Thr

35

40

45

Gly Met Val Leu Val Gly Gly Glu Ile Thr Thr Ser Ala Trp Val Asp

50

55

60

Ile Glu Glu Ile Thr Arg Asn Thr Val Arg Glu Ile Gly Tyr Val His

65

70

75

80

Ser Asp Met Gly Phe Asp Ala Asn Ser Cys Ala Val Leu Ser Ala Ile

85

90

95

Gly Lys Gln Ser Pro Asp Ile Asn Gln Gly Val Asp Arg Ala Asp Pro

100

105

110

Leu Glu Gln Gly Ala Gly Asp Gln Gly Leu Met Phe Gly Tyr Ala Thr

115

120

125

Asn Glu Thr Asp Val Leu Met Pro Ala Pro Ile Thr Tyr Ala His Arg

130

135

140

Leu Val Gln Arg Gln Ala Glu Val Arg Lys Asn Gly Thr Leu Pro Trp

145

150

155

160

Leu Arg Pro Asp Ala Lys Ser Gln Val Thr Phe Gln Tyr Asp Asp Gly  
165 170 175

Lys Ile Val Gly Ile Asp Ala Val Val Leu Ser Thr Gln His Ser Glu  
180 185 190

Glu Ile Asp Gln Lys Ser Leu Gln Glu Ala Val Met Glu Glu Ile Ile  
195 200 205

Lys Pro Ile Leu Pro Ala Glu Trp Leu Thr Ser Ala Thr Lys Phe Phe  
210 215 220

Ile Asn Pro Thr Gly Arg Phe Val Ile Gly Gly Pro Met Gly Asp Cys  
225 230 235 240

Gly Leu Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly Gly Met Ala  
245 250 255

Arg His Gly Gly Ala Phe Ser Gly Lys Asp Pro Ser Lys Val Asp  
260 265 270

Arg Ser Ala Ala Tyr Ala Ala Arg Tyr Val Ala Lys Asn Ile Val Ala  
275 280 285

Ala Gly Leu Ala Asp Arg Cys Glu Ile Gln Val Ser Tyr Ala Ile Gly  
290 295 300

Val Ala Glu Pro Thr Ser Ile Met Val Glu Thr Phe Gly Thr Glu Lys  
305 310 315 320

Val Pro Ser Glu Gln Leu Thr Leu Leu Val Arg Glu Phe Phe Asp Leu  
325 330 335

Arg Pro Tyr Gly Leu Ile Gln Met Leu Asp Leu Leu His Pro Ile Tyr  
340 345 350

Lys Glu Thr Ala Ala Tyr Gly His Phe Gly Arg Glu His Phe Pro Trp  
355 360 365

Glu Lys Thr Asp Lys Ala Gln Leu Leu Arg Asp Ala Ala Gly Leu Lys  
370 375 380

<210> 2

<211> 1155

<212> DNA

<213> Escherichia coli

<220>

<221> gene

<222> (1)..(1152)

<223> metK

<300>

<301> Blattner, F. R.

<302> The complete genome sequence of Escherichia coli K-12.

<303> Science

<304> 277

<306> 1453-1474

<307> 1997

<400> 2

atggcaaaac accttttac gtccgagtcc gtctctgaag ggcattctga caaaattgct 60

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gcttgcgaaa cctacgtaaa aaccggcatg gttttagttg gcggcgaaat caccaccagc 180

gcctgggtag acatcgaaga gatcaccgtt aacaccgttc gcgaaattgg ctatgtcat 240

tccgacatgg gctttgacgc taactcctgt gcgggtctga gcgctatcgaaaacagtct 300  
cctgacatca accagggcgt tgaccgtgcc gatccgctgg aacagggcgc gggtgaccag 360  
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ctgcgcccgg acgcgaaaag ccaggtgact tttcagtatg acgacggcaa aatcggttgt 540  
atcgatgctg tcgtgctttc cactcagcac tctgaagaga tcgaccagaa atcgctgcaa 600  
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accaaattct tcatcaaccc gaccggtcgt ttcgttatcg gtggccaaat gggtgactgc 720  
ggtctgactg gtcgtaaaat ttcgttgat acctacggcg gcatggcgctc acgggtggc 780  
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tacgcaatcg gcgtggctga accgacctcc atcatggtag aaactttcg 960

gtgccttctg aacaactgac cctgctggta cgtgagttct tcgacctgcg cccatacg 1020

ctgattcaga tgctggatct gctgcacccg atctacaaag aaaccgcagc atacggtcac 1080

tttggtcgtg aacatttccc gtggaaaaaa accgacaaag cgca gctgcgatgct 1140

gccggtctga agtaa 1155

<210> 3

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Oligonucleotide metK2

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ccttaattaa tgtctgttgt ggttggtgt

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<210> 4

<211> 29

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Oligonucleotide metK4

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ggaattctct ttaggaggta ttaaatatg

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<210> 5

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Oligonucleotide RLSS1

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37

<210> 6

<211> 40

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Oligonucleotide RLSS2

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<210> 7

<211> 33

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Oligonucleotide GAPDHfw

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<210> 8

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligonucleotide GAPDHrevII

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<210> 9

<211> 46

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Multiple Cloning Site

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<210> 10

<211> 1185

<212> DNA

<213> *Rattus norvegicus*

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<221> CDS

<222> (1)..(1185)

<223> RLSS-Gen

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gcc ttc atg ttc aca tct gaa tcg gta gga gaa ggg cat cca gat aag 96  
Ala Phe Met Phe Thr Ser Glu Ser Val Gly Glu Gly His Pro Asp Lys

20 25 30

atc tgt gac cag att agt gat gca gtg ctg gat gcc cat ctc aag caa 144  
Ile Cys Asp Gln Ile Ser Asp Ala Val Leu Asp Ala His Leu Lys Gln

35 40 45

gac ccc aat gcc aag gtg gcc tgt gag aca gtg tgc aag aca ggg atg 192  
Asp Pro Asn Ala Lys Val Ala Cys Glu Thr Val Cys Lys Thr Gly Met

50 55 60

gtg ctc ctg tgt gga gag atc acc tca atg gcc atg att gac tac cag 240  
Val Leu Cys Gly Glu Ile Thr Ser Met Ala Met Ile Asp Tyr Gln  
65 70 75 80

cgg gtg gtg aga gac acc att aag cac att ggc tac gat gac tct gcc 288  
Arg Val Val Arg Asp Thr Ile Lys His Ile Gly Tyr Asp Asp Ser Ala  
85 90 95

aag ggc ttc gac ttc aag acc tgc aat gtg ctc gtg gct ctg gag caa 336  
Lys Gly Phe Asp Phe Lys Thr Cys Asn Val Leu Val Ala Leu Glu Gln  
100 105 110

cag tcc cca gac att gcc caa tgt gtc cat cta gac aga aat gag gag 384  
Gln Ser Pro Asp Ile Ala Gln Cys Val His Leu Asp Arg Asn Glu Glu  
115 120 125

gac gtt ggt gca gga gat cag ggt ctg atg ttc ggc tat gcc act gac 432  
Asp Val Gly Ala Gly Asp Gln Gly Leu Met Phe Gly Tyr Ala Thr Asp  
130 135 140

gag aca gag gag tgc atg ccg ctc acc att gtt ctt gct cac aaa ctc 480  
Glu Thr Glu Glu Cys Met Pro Leu Thr Ile Val Leu Ala His Lys Leu

145 150 155 160  
aac acc cgg atg gca gat ctg agg cgc tct ggt gtc ctt ccc tgg ctg 528  
Asn Thr Arg Met Ala Asp Leu Arg Arg Ser Gly Val Leu Pro Trp Leu  
165 170 175  
aga cct gat tct aag act cag gta aca gtt cag tac gtg cag gat aat 576  
Arg Pro Asp Ser Lys Thr Gln Val Thr Val Gln Tyr Val Gln Asp Asn  
180 185 190  
ggt gct gtc atc cct gtt cgc gtc cac acc atc gtc atc tct gtg caa 624  
Gly Ala Val Ile Pro Val Arg Val His Thr Ile Val Ile Ser Val Gln  
195 200 205  
cac aac gaa gac ata aca ctg gag gcc atg cga gag gcc ctg aag gag 672  
His Asn Glu Asp Ile Thr Leu Glu Ala Met Arg Glu Ala Leu Lys Glu  
210 215 220  
cag gtg atc aaa gct gtg gtg cca gcc aag tac ctg gat gaa gac acc 720  
Gln Val Ile Lys Ala Val Val Pro Ala Lys Tyr Leu Asp Glu Asp Thr  
225 230 235 240

atc tac cac ctg cag cca agt ggg cgg ttt gtc atc gga ggt ccc cag 768  
Ile Tyr His Leu Gln Pro Ser Gly Arg Phe Val Ile Gly Gly Pro Gln  
245 250 255

ggg gat gca ggt gtc aca ggc cgc aag att att gtg gac aca tac gga 816  
Gly Asp Ala Gly Val Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly  
260 265 270

ggc tgg ggt gcc cat ggt ggt gcc ttc tct gga aag gac tac acc 864  
Gly Trp Gly Ala His Gly Gly Ala Phe Ser Gly Lys Asp Tyr Thr  
275 280 285

aag gtg gac cgc tca gca gct tat gcc gcc cgc tgg gtg gcc aag tct 912  
Lys Val Asp Arg Ser Ala Ala Tyr Ala Ala Arg Trp Val Ala Lys Ser  
290 295 300

ctg gtg aag gct ggg ctc tgc cgg aga gtc ctt gtt cag gtg tcc tat 960  
Leu Val Lys Ala Gly Leu Cys Arg Arg Val Leu Val Gln Val Ser Tyr  
305 310 315 320

gcc att ggt gtg gca gaa cct ctg tcc att tcc att ttc acc tac gga 1008  
Ala Ile Gly Val Ala Glu Pro Leu Ser Ile Ser Ile Phe Thr Tyr Gly

325

330

335

act tcc aag aag acc gag cga gag cta cta gag gtt gtg aac aag aac 1056

Thr Ser Lys Lys Thr Glu Arg Glu Leu Leu Glu Val Val Asn Lys Asn

340

345

350

ttt gac ctc cgg ccg ggt gtt att gtc agg gac ttg gat ctg aag aag 1104

Phe Asp Leu Arg Pro Gly Val Ile Val Arg Asp Leu Asp Leu Lys Lys

355

360

365

ccc atc tac cag aag act gca tgc tat ggt cat ttc gga aga agc gag 1152

Pro Ile Tyr Gln Lys Thr Ala Cys Tyr Gly His Phe Gly Arg Ser Glu

370

375

380

ttt ccc tgg gag gtc ccc aag aag ctt gtg ttt 1185

Phe Pro Trp Glu Val Pro Lys Lys Leu Val Phe

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<210> 11

<211> 395

<212> PRT

<213> *Rattus norvegicus*

<400> 11

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1 5 10 15

Ala Phe Met Phe Thr Ser Glu Ser Val Gly Glu Gly His Pro Asp Lys

20 25 30

Ile Cys Asp Gln Ile Ser Asp Ala Val Leu Asp Ala His Leu Lys Gln

35 40 45

Asp Pro Asn Ala Lys Val Ala Cys Glu Thr Val Cys Lys Thr Gly Met

50 55 60

Val Leu Leu Cys Gly Glu Ile Thr Ser Met Ala Met Ile Asp Tyr Gln

65 70 75 80

Arg Val Val Arg Asp Thr Ile Lys His Ile Gly Tyr Asp Asp Ser Ala

85 90 95

Lys Gly Phe Asp Phe Lys Thr Cys Asn Val Leu Val Ala Leu Glu Gln

100 105 110

Gln Ser Pro Asp Ile Ala Gln Cys Val His Leu Asp Arg Asn Glu Glu

115 120 125

Asp Val Gly Ala Gly Asp Gln Gly Leu Met Phe Gly Tyr Ala Thr Asp

130 135 140

Glu Thr Glu Glu Cys Met Pro Leu Thr Ile Val Leu Ala His Lys Leu

145 150 155 160

Asn Thr Arg Met Ala Asp Leu Arg Arg Ser Gly Val Leu Pro Trp Leu

165 170 175

Arg Pro Asp Ser Lys Thr Gln Val Thr Val Gln Tyr Val Gln Asp Asn

180 185 190

Gly Ala Val Ile Pro Val Arg Val His Thr Ile Val Ile Ser Val Gln

195 200 205

His Asn Glu Asp Ile Thr Leu Glu Ala Met Arg Glu Ala Leu Lys Glu

210 215 220

Gln Val Ile Lys Ala Val Val Pro Ala Lys Tyr Leu Asp Glu Asp Thr

225 230 235 240

Ile Tyr His Leu Gln Pro Ser Gly Arg Phe Val Ile Gly Gly Pro Gln

245 250 255

Gly Asp Ala Gly Val Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly

260 265 270

Gly Trp Gly Ala His Gly Gly Ala Phe Ser Gly Lys Asp Tyr Thr

275 280

285

Lys Val Asp Arg Ser Ala Ala Tyr Ala Ala Arg Trp Val Ala Lys Ser

290 295 300

Leu Val Lys Ala Gly Leu Cys Arg Arg Val Leu Val Gln Val Ser Tyr

305 310 315 320

Ala Ile Gly Val Ala Glu Pro Leu Ser Ile Ser Ile Phe Thr Tyr Gly

325 330 335

Thr Ser Lys Lys Thr Glu Arg Glu Leu Leu Glu Val Val Asn Lys Asn

340 345 350

Phe Asp Leu Arg Pro Gly Val Ile Val Arg Asp Leu Asp Leu Lys Lys

355 360 365

Pro Ile Tyr Gln Lys Thr Ala Cys Tyr Gly His Phe Gly Arg Ser Glu

370 375 380

Phe Pro Trp Glu Val Pro Lys Lys Leu Val Phe

385

390

395